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Genetic Diversity Studies in Aromatic Rice (*Oryza Sativa L.*) Germplasm

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The genetic divergence study conducted with 50 rice genotypes comprising both Basmati and aromatic short grain types revealed significant differences among the genotypes for the yield, its components and grain quality characteristics. Based on the relative magnitude of D^2 values, the genotypes were grouped into eight clusters by both Tocher's and Euclidian methods of divergence study. Among all the clusters, cluster IV was the largest one with 12 genotypes, whereas cluster VIII had only one genotype (Pusa 1121). The cluster VIII was separated by higher genetic distance from cluster III and II followed by cluster V. Cluster VIII with only one genotype (Pusa 1121) exhibited the highest mean value for kernel length, kernel length after cooking and 1000- grain weight. Cluster VII possessed the highest mean value for kernel length, L/B ratio and kernel length after cooking due to inclusion of the most promising genotypes like Pusa Sugandh-3, Sugandhamathi and Basmati- 386, which are known for good quality traits. Cluster V containing genotypes, Gahansal, Chitti mutyalu and Godavari Isukalu exhibited good performance for most of the characters and registered more number of grains per panicle. Based on the inter cluster distances and other desirable attributes, crossing between Pusa 1121, JGL 15336, RNR 2465, Badsha bhog, NDR 6242, Gahansal and Chitti mutyalu is suggested for further improvement in grain quality and yield.

Keywords: Aromatic rice, Genetic divergence, D^2statistics, Cluster analysis, PC

Aromatic rice constitute a special group of accessions well known for its aroma and superfine grain quality (Nene 1998; Singh *et al*. 2000a,b). Basmati rice has been the food of choice for rich people for centuries. Aromatic rice has occupied a prime position in Indian society, not only for high quality, but also considered auspicious. Modern methods of information technology and awareness about its unique palatability and easy digestibility have expanded the demand even to common man. Every year domestic, as well as international demand is on the rise. Basmati exports are the major source of addition to annual national exchequer. India, one of the major exporters of Basmati rice is well known for its immense diversity of aromatic rice varieties.

As per the growing demand of aromatic rice, the emphasis should be given for the development of high yielding, fine grain aromatic rice with outstanding quality traits like aroma, kernel elongation after cooking, fluffiness and taste. The diversity in crop genetic resources and its understanding is essential for crop improvement in terms of increasing food production. Study of genetic divergence among the plant materials is a vital tool to the plant breeder for an efficient choice of parents for crop improvement. Genetically diverse parents are likely to contribute desirable segregants and/or high heterotic crosses.

Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis' D^2-statistic has been proved to be a powerful technique (Murty and Arunachalam, 1966). It provides a quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1936). In the present investigation, an attempt was made to classify the extent of genetic diversity for certain yield and quality traits in scented rice genotypes for ultimate use in hybridization programme.

Materials and Methods

Fifty germplasm lines containing both Basmati and aromatic short grain types (Table 1) available at Rice section (AICRIP), Agricultural Research Institute, Rajendranagar, Hyderabad were used during kharif, 2009 to estimate the genetic divergence.

Observations were recorded for days to 50 per cent flowering, plant height(cm), number of productive tillers per plant, panicle length(cm), number of grains per panicle, number of filled

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Table 1. Details of aromatic rice genotypes

Genotype	Source/Cross combination
Jeerakasala	Land race from Kerala
Gandasala	Land race from Kerala
CR 2616- 3-3-3-1	Pusa 44/ Dubraj
RNR 2465	RNR –M 7/ RNR 19994
KJT-4-4-36-12-13-29	KJT 9-333/ Indrayani
JGL 15281	JGL 4870 / Godavari Isukalu
JGL 15336	JGL 384 / Godavari Isukalu
NDR 6235	Selection from Kalanamak Basti
NDR 6242	Selection from Kalanamak Birdpur
Ranbir Basmati	Selection from Basmati 370
Narendra lalmatti	Selection from Local lalmatti
NDR 8018	BKP 246 / Sabita // IR 40931-33-1-B-2
Pusa 1121	Pusa 614-1-2 / Pusa 614-2-4-3
Kasturi	Basmati 370 / CRR 88-17-1-5
NDR 9542	BKP 242 / NDR 30030 // Swarna
MahiSugandha	BK 79 / Basmati 370
Vasumati	PR 109 / Pak Basmati
Haryana Basmati	Sona / Basmati 370
Geetanjali	Mutant from Basmati 370
Sugandhamati	Pusa Basmati -1 / IET 12603
Pusa Basmati	Pusa 150/ Karnal local
Pusa Sugandh -3	Pusa 2504-1-3-1
NDR 8428-1-2	PSBRC 68 / Kalanamak
NDR 9539	BPT 5204 / Kalanamak
HUR-ASG-GR-32-87 S	Selection from Gr-32
ASH 4022	Material from ASG trial
HUR-ASG-KN-23 S	Selection from Kalanamak collected from Nawgarh
CR 2600	NDR 8015 / Dubraj
CR 2603	NDR 8095 / Dubraj
CR 2613 -1-1-1-5-1	KJ / RP
CR 2615 -1	KK Selection
CR 2613 -1-5-2-5-1	KJ / RP
Badshabhog	Local selection
Kalanamak	Local selection
AS – 100	Material from ASG trial
Pak Basmati	Local selection
Basmati 386	Selection from Pak Basmati
Basmati 370	Selection from Pak Basmati
ASG- 4013	Material from ASG trial
Yamini	Bhurarata 4-10 / Pak Basmati
Taroari Basmati	Pure line selection from HBC 19
Chitti mutyalu	Local land race of Andhra Pradesh
Godavari Isukalu	Local land race of Andhra Pradesh
Sumati	Chandan / Pak Basmati
RNR 19186	BPT 5204 / Tella hamsa
RNR 22629	Kavya / Pusa Basmati
RNR 2009312	RNR 5997 / Kasturi
RNR 16511	Chandan / Pak Basmati
RNR 17818	WGL 48684 / Pusa Basmati
Gahansal	Local land race of Maharastra

grains per panicle, 1000-grain weight (g), harvest index, grain yield per plant(g) and for grain quality characters *viz*; kernel length, kernel breadth, L/B ratio, kernel length after cooking, kernel elongation ratio and volume expansion ratio. Analysis of variance was computed as per standard statistical procedure (Panse and Sukhatme, 1978). A measure for group distance based on multiple characters was given following Mahalanobis (1936) using D^2 statistic to compute genetic divergence between genotypes. Each character was ranked on the basis of its combination towards divergence between two entries ($di = r_t^i - r_t^j$). Rank 1 was given to the highest mean difference and rank P to the lowest difference. For grouping of varieties into various clusters, two methods namely, Tocher and Euclidean method (Rao, 1952) have been used.

Results and Discussion

Analysis of variance revealed highly significant differences among the genotypes for all the traits under study, indicating the variability among the genotypes (Table.2).

Table 2. Analysis of variance for yield and quality traits

Character	Mean sum of squares
	Treatments
Days to 50% flowering	99.633 **
Plant height	2251.34**
Number of productive tillers per plant	62.171**
Panicle length	18.06**
Number of grains per panicle	10599.49**
Number of filled grains per panicle	8031.93**
1000-grain weight	59.67**
Grain yield per plant	92.66**
Harvest index	105.60**
Kernel length	5.29**
Kernel breadth	0.068
L/B ratio	1.77*
Kernel length after cooking	21.49
Kernel elongation ratio	0.33
Volume expansion ratio	1.44**

** Significant at 1 per cent level; *Significant at 5 per cent level

Information about nature and degree of divergence would help the plant breeder in choosing the right type of parents for further breeding programme to improve the produce quality and yield traits. Hence, estimation of genetic diversity in yield and grain quality parameters among genotypes is important for planning the crossing programme. Fifty genotypes of aromatic rice were grouped into eight clusters (Table.3 and Fig.1) based on relative magnitude of D^2 values.

Table 3. Clustering pattern among 50 aromatic rice genotypes (D^2 analysis)

Cluster No	No. of genotypes	Names of the genotypes
I	7	KJT-4 -4-36-12-13-29, NDR 8018, Narendra lalmatti , NDR 9542, CR 2613-1-1-1-5-1, Kasturi , CR 2613-1-5-2-5-1.
II	4	JGL15281, JGL 15336, RNR 2465, CR 2616-3-3-3-1.
III	6	CR2615-1, Badsha bhog, , NDR 9539, NDR 6242, AS-100, Gandasala.
IV	12	NDR 6235, Kalanamak , Jeerakasala, NDR 8428-1-2, HUR ASG GR 32-87 S , CR 2600, CR 2603, Ranbir Basmati, ASH 4022 , HUR ASG KN 23 S, Yamini , Taroari Basmati.
V	4	Godavari Isukalu, Gahansal, ASG -4013, Chitty mutyalu.
VI	9	Mahi Sugandha, Haryana Basmati , Pusa Basmati, RNR 22629, RNR2009312, RNR16511, Sumati, RNR 19186, RNR17818.
VII	7	Vasumati , Pak Basmathi , Geetanjali, Sugandhamati, Pusa Sugandh -3, Basmati 370, Basmati 386
VIII	1	Pusa 1121

The cluster IV was the largest one with 12 genotypes; cluster VI with nine genotypes, cluster I

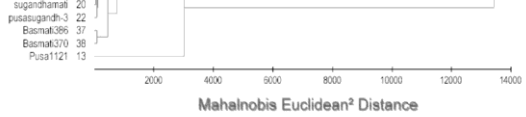

Fig. 1. Cluster diagram representing diversity for 50 genotypes of aromatic rice

and VII with seven genotypes each, cluster III with 6 genotypes, cluster II and V with four genotypes each, while, cluster VIII had only one genotype.

Fig. 2. Clustering pattern (Ward's minimum variance dendrogram)

The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. This suggested that forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the evolution of diversity of genotypes. Variation in environment could also be responsible for this diversity. Similar conclusions have been drawn by several workers *viz*., Rao and Gomatinayagam (1997), Pandey *et al*. (1999), Hegde and Patil (2000), Rather *et al*. (2001), Vanaja *et al*. (2003), Nayak *et al*. (2004), Arun Sharma *et al*. (2008), Ansari *et al* (2010), Bhadru *et. al*., (2012) and Praveen singh *et al* (2012). The clustering pattern of genotypes indicated existence of significant amount of variability, which was in conformation with the findings of Soni *et al*. (1999) and Ahmed *et al* (2010).

Table 4. Intra (diagonal) and Inter cluster distances

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	241.12	496.99	583.33	532.66	885.55	912.37	1635.77	7618.14
Cluster II		271.9	531.83	982.13	883.57	1675.19	2589.81	9461.71
Cluster III			328.66	733.17	909.25	1830.82	2801.81	9933.74
Cluster IV				332.63	787.22	741.04	1240.96	6434.49
Cluster V					634.21	1166.42	1947.34	7649.21
Cluster VI						245.1	420.12	3959.08
Cluster VII							276.23	2597.3
Cluster VIII								0

Though D ^{2}statistics using Tocher method for classifying the genotypes is useful non-hierarchical Euclidian cluster analysis (based on Wards minimum variance dendrogram) (Figure 2) critically identifies sub clusters of the major groups at different levels. Maximum intra cluster distance was observed (Table 4) (Fig.2) in cluster V (634.21), followed by cluster IV (332.63) and cluster III (328.66). Thus, selection of genotypes based on high *per se* and other desirable traits from cluster IV, which had maximum number of genotypes (12) might be helpful to generate useful breeding materials. Minimum intra cluster distance in cluster VIII indicated the limited genetic diversity.

Based on inter cluster distance, cluster VIII, which has one genotype was separated by higher genetic distance from cluster III and II. Another cluster VII was divergent from the clusters III and II, followed by cluster V. The hybrids developed from the selected members on the basis of D ^{2}matrix value would produce highly variable population in the segregating generations.

A wide range of variation was registered in the cluster means for most of the characters studied (Table.5). Higher differences in the mean values were observed for plant height, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, 1000-grain weight, grain yield per plant, harvest index and kernel length after cooking, whereas for the characters like days to 50 per cent flowering, harvest index, panicle length, kernel length, kernel breadth, L/B ratio, kernel elongation ratio and volume expansion ratio, the variation was low.

The genotypes included in cluster I were dwarf types with moderate kernel length. Cluster II exhibited the lowest mean value for plant height and highest mean values for number of grains per panicle, number of filled grains per panicle, harvest index, kernel elongation ratio and the lines included were RNR 2465 and JGL 15281. Cluster III with six genotypes exhibited the highest mean value for panicle length, number of grains per panicle and harvest index. Cluster IV exhibited the highest value

for plant height, panicle length, grain yield per plant and kernel length. Cluster V containing genotypes, *viz*., Gahansal, Chitti mutyalu and Godavari Isukalu exhibited good performance for most of the characters and was mostly characterized by more number of grains per panicle, number of filled grains per panicle, number of productive tillers per plant and grain yield per plant. Cluster VI was not identified for any specific feature, hence, considered as average. Among all the clusters, Cluster VII posseses the highest mean for kernel length, L/B ratio and kernel length after cooking, because of presence of promising genotypes like Pusa Sugandh-3, Sugandamati and Basmati 386 for quality traits. Cluster VIII consisting only one genotype (Pusa 1121) exhibited the highest mean for kernel length after cooking, kernel length, 1000-grain weight and the lowest mean for days to 50 per cent flowering and plant height. It is observed that no single cluster contained unique genotype with all desirable traits, which ruled out the possibility of selecting directly for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. Among 15 characters including yield that are considered for the estimation of genetic divergence, four characters were considered to be potential contributors for genetic divergence (Table 6). The maximum genetic divergence was contributed by kernel length after cooking (61.31%),followed by plant height (10.94%),volume expansion ratio (8.08%), number of productive tillers per plant (7.18%) and these results are in conformity with the findings of Surender Raju (2002), Nayak *et al*. (2004) and Shobha Rani *et.al*.(2012).

Table 5. Cluster means for yield components and quality traits (D^2analysis)

Parameters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50% flowering	100	102	103.61	100.47	108.33	103.92	100.52	97
Plant height	103.09	100.48	155.1	155.14	140.06	107.11	112.48	114.06
Number of productive tillers per plant	10.12	9.78	11.18	13.17	21.19	15.54	12.81	12.55
Panicle length	24.6	21.62	27.16	26.36	26.15	26.12	25.28	26.02
Number of grains per panicle	183.51	245.81	232.76	169.95	292.36	199.59	166.08	94.2
Number of filled grains per panicle	129.25	204.36	195.53	146.23	219.98	129.81	122.59	82
1000-grain weight	18.18	12.15	14.67	19.42	15.23	19.83	22.15	25.62
Grain yield per plant	16.13	20.13	22.02	24.62	25.04	18.07	18.61	11.55
Harvest index	40.48	44.7	40.07	40.79	41.27	40.83	39.63	25.45
Kernel length	6.05	4.02	4.74	6.17	4.18	7.04	7.48	8.34
Kernel breadth	1.9	1.89	2.08	2	1.92	1.86	1.85	1.93
L/B ratio	3.15	2.13	2.32	3.1	2.17	3.79	3.96	4.31
Kernel length after cooking	8.88	8.24	7.39	9.81	9.98	12.39	13.9	20.83
Kernel elongation ratio	1.48	2.08	1.64	1.61	2.38	1.76	1.86	2.5
Volume expansion ratio	4.43	4.8	4.55	4.21	3.52	3.91	4.55	4.27

Table 6. Relative contribution of different traits towards genetic divergence in scented rice

Characters	No. of times ranked first	Contribution (%)
Days to 50% flowering	7	0.57
Plant height	134	10.94
Number of productive tillers per plant	88	7.18
Panicle length	0	0.00
Number of grains per panicle	6	0.49
Number of filled grains per panicle	1	0.08
1000-grain weight	29	2.37
Grain yield per plant	5	0.41
Harvest index	0	0.00
Kernel length	57	4.65
Kernel breadth	20	1.63
L/B ratio0	0.00	
Kernel length after cooking	751	61.31
Kernel elongation ratio	28	2.29
Volume expansion ratio	99	8.08

Canonical root analysis was used to confirm the clustering pattern obtained by D^2statistics to plot the genotypes on two or three dimensional graphs. The canonical root analysis in the present study accounted for the total variance of 77.82 per cent (Table 7) by 5 principal components.

Table 7. Eigen values and percentage of variation for corresponding 15 component characters

Parameter	PC_1	PC_2	PC_3	PC_4	PC_5
Eigen value of canonical root	4.99	2.69	1.96	1.12	0.89
Percentage of variation observed	33.28	17.95	13.11	7.52	5.94
Cumulative total per cent variation	33.28	51.23	64.35	71.87	77.82
Days to 50% flowering	0.092	0.147	0.288	0.499	0.613
Plant height	0.125	0.542	-0.131	-0.15	-0.014
No. of productive tillers/ plant	-0.071	0.244	0.395	0.349	-0.511
Panicle length	-0.019	0.337	0.414	-0.348	0.004
No. of grains/ panicle	0.294	0.064	0.268	0.088	-0.452
No. of filled grains/ panicle	0.174	0.442	-0.294	-0.115	-0.01
1000-grain weight	-0.357	0.233	0.037	0.191	-0.062
Grain yield/ plant	0.265	0.294	-0.051	0.006	0.225
Harvest index	0.303	-0.18	0.204	-0.205	-0.069
Kernel length	-0.411	0.02	0.01	-0.117	-0.001
Kernel breadth	-0.284	0.369	-0.174	0.023	0.007
Length/ breadth Ratio	-0.299	-0.003	0.289	0.023	0.045
Kernel length after cooking	-0.335	-0.022	0.148	0.066	0.122
Kernel elongation ratio	0.337	0.033	0.145	0.317	0.108
Volume expansion ratio	-0.01	-0.025	-0.46	0.516	-0.266

The contribution of PC1, PC2 and PC3, PC4 and PC5 was 33.28 per cent, 17.95 per cent 13.11 per cent, 7.52 per cent and 5.94 per cent, respectively. The first canonical root accounted for 33.28 per cent of total variance of uncorrelated variables indicating the differentiation of these traits in these genotypes was complete in three phases. The relative contribution of genotypes reflected in the existence of broad parallelism between groups obtained by D^2analysis and vector analysis. For getting clear association of two dimensional representation of variation, the first three canonical roots should be more than 95 per cent. On the contrary, the two vectors as a whole contributed only 51.23 per cent towards genetic divergence because of which

discernable overlapping was observed in group constellations of canonical vectors.

The characters like kernel elongation ratio, harvest index, number of grains per panicle, grain yield per plant, plant height contributed maximum towards genetic divergence in the first vector. In the second vector, plant height, number of filled grains per panicle, kernel breadth, panicle length, grain yield per plant, number of productive tillers per plant,1000-grain weight, days to 50 per cent flowering, number of grains per panicle, kernel elongation ratio and kernel length contributed maximum towards genetic diversity. Panicle length, number of productive tillers per plant, L/B ratio, days to 50 per cent flowering, number of grains per panicle, harvest index, kernel length after cooking, kernel elongation ratio, 1000-grain weight and kernel length contributed much towards genetic divergence in third vector. In the fourth vector, volume expansion ratio, days to 50 per cent flowering, number of productive tillers per plant, kernel elongation ratio,1000- grain weight, number of grains per panicle, kernel length after cooking, kernel breadth, L/B ratio and grain yield per plant contributed maximum towards genetic diversity. Days to 50 per cent flowering, grain yield per plant, kernel length after cooking, kernel elongation ratio, L/B ratio, kernel breadth and panicle length contributed maximum to the genetic diversity in the fifth vector. This was also in conformity with the relative contribution of characters through D^2statistics and similar type of study was also carried out by Siddique *et. al* (2010), Maji and Saibu (2012) and Praveen Singh *et. al* (2012).

From the entire study, it can be concluded that kernel length, kernel breadth, days to 50 per cent flowering, kernel elongation ratio, number of grains per panicle and number of productive tillers per plant are the important traits contributing towards genetic divergence and for discriminating genotypes. Based on the inter cluster distances and high *per se* performance for the desirable attributes, crossing between the genotypes *viz.*, Pusa 1121 of cluster VIII, JGL 15336, RNR 2465 of cluster II and Badsha bhog, NDR 6242 of cluster III, Gahansal, Chitti mutyalu and Godavari Isukalu of cluster V and Pusa Sugandh-3, Sugandamati and Basmati 386 in cluster VII can be used for improvement of grain yield and quality traits.

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